

# Chromosome segregation model - detailed description

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## Introduction

This is a more detailed version of the kinetochore segregation model to be published in the JCB article, which should be referred to for all the experimental, biological and non-technical aspects of this work.

## 1 Definitions

### 1.1 State vector

The mitotic spindle is described by the speeds and position along the  $x$  axis of two spindle pole bodies,  $N$  chromosomes with two centromeres and  $M_k$  attachment sites per centromere.

Positions are noted as follow:

- The left and right spindle pole bodies ( SPBs ),  $x_s^L$  and  $x_s^R$
- The  $N$  centromeres,  $x_n^A, x_n^B, n \in \{1, \dots, N\}$
- The  $M_k$  attachment sites of each centromere,  $x_{nm}^A, x_{nm}^B, n \in \{1, \dots, N\}, m \in \{1, \dots, M_k\}$

The speeds are noted with a dot:  $dx/dt = \dot{x}$ .

As all the interactions are assumed to be parallel to the spindle axis, only the positions along this axis are considered, in a coordinate system with its origin at the center of the spindle, which means that  $x_s^L(t) = -x_s^R(t) \forall t$ .

### 1.2 Random variables for the attachment

We define  $\rho_{nm}^A$  and  $\lambda_{nm}^A$ , two random variables that govern the attachment state of the site  $x_{nm}^A$ , such that:

$$\lambda_{nm}^A = \begin{cases} 1 & \text{if the site is attached to the left SPB} \\ 0 & \text{otherwise} \end{cases} \quad (1)$$

$$\rho_{nm}^A = \begin{cases} 1 & \text{if the site is attached to the right SPB} \\ 0 & \text{otherwise} \end{cases} \quad (2)$$

Note that  $\rho_{nm}^A$  and  $\lambda_{nm}^A$  are not independent, as an attachment site can't be attached to both poles. To take this into account, we can define the variable  $\pi_{nm}^A = \rho_{nm}^A - \lambda_{nm}^A$  such that:

$$\pi_{nm}^A = \begin{cases} -1 & \text{if the site is attached to the left SPB} \\ 0 & \text{if the site is not attached} \\ 1 & \text{if the site is attached to the right SPB} \end{cases} \quad (3)$$

We have:

$$\lambda_{nm}^A = \pi_{nm}^A (\pi_{nm}^A - 1) / 2 \quad (4)$$

$$\rho_{nm}^A = \pi_{nm}^A (\pi_{nm}^A + 1) / 2 \quad (5)$$

We also define  $N_n^{AL}$  and  $N_n^{AR}$  as the number of ktMTs of centromere A attached to the left and right SPBs, respectively:

$$N_n^{AL} = \sum_{m=1}^{M_k} \lambda_{nm}^A \text{ and } N_n^{AR} = \sum_{m=1}^{M_k} \rho_{nm}^A \quad (6)$$

Note that  $N_n^{AL} + N_n^{AR} \leq M_k \forall \pi_{nm}$ . The same definitions apply for the centromere B and left SPB.

## 2 Mechanical system

### 2.1 Forces

The following force balances are considered:

#### 2.1.1 Forces at the left SPB :

Because of the reference frame definition,  $\dot{x}_s^R = -\dot{x}_s^L \forall t$ . Here we substituted  $x_s^L$  with  $-x_s^R$

- Friction forces (viscous drag):  $F_f^L = \mu_s \dot{x}_s^R$

- Midzone force generators:

$$F_{mid}^L = -F_z (1 - 2\dot{x}_s^R / V_z)$$

- Total kinetochore microtubules force generators:

$$F_{kMT}^T = \sum_{n=1}^N \sum_{m=1}^{M_k} -\lambda_{nm}^A F_k (1 + (\dot{x}_{nm}^A + \dot{x}_s^R) / V_k) \\ - \lambda_{nm}^B F_k (1 + (\dot{x}_{nm}^B + \dot{x}_s^R) / V_k)$$

#### 2.1.2 Forces at the right SPB :

- Friction forces (viscous drag):  $F_f^R = -\mu_s \dot{x}_s^R$

- Midzone force generators:

$$F_{mid} = F_z (1 - (\dot{x}_s^R - \dot{x}_s^L) / V_z) = F_z (1 - 2\dot{x}_s^R / V_z)$$

- Total kinetochore microtubules force generators:

$$F_{kMT}^T = \sum_{n=1}^N \sum_{m=1}^{M_k} -\rho_{nm}^A F_k (1 - (\dot{x}_{nm}^A - \dot{x}_s^R) / V_k) \\ - \rho_{nm}^B F_k (1 - (\dot{x}_{nm}^B - \dot{x}_s^R) / V_k)$$

### 2.1.3 Forces at centromere $An$

- Drag:  $F_c^f = -\mu_c \dot{x}_n^A$
- Cohesin bond (Hook spring) restoring force exerted by centromere<sup>1</sup>:

$$F_{BA} = \begin{cases} \kappa_c(x_n^B - x_n^A - d_0) & \text{if } x_n^A \leq x_n^B \\ \kappa_c(x_n^B - x_n^A + d_0) & \text{if } x_n^A > x_n^B \end{cases} \quad (7)$$

With  $F_{AB} = -F_{BA}$ .

- Total visco-elastic bond between the centromere A and the attachment sites:

$$F_v^T = \sum_{m=1}^{M_k} -\kappa_k(x_n^A - x_{nm}^A) - \mu_k(\dot{x}_n^A - \dot{x}_{nm}^A)$$

### 2.1.4 Forces at attachment site $Anm$

- Visco-elastic bond between the centromere A and the attachment sites:

$$F_v = \kappa_k(x_n^A - x_{nm}^A) + \mu_k(\dot{x}_n^A - \dot{x}_{nm}^A)$$

- Kinetochore microtubules force generators:

$$\begin{aligned} F_{kMT}^A &= F_{kMT}^{RA} + F_{kMT}^{LA} \\ F_{kMT}^{RA} &= \rho_{nm}^A F_k \left( 1 - \frac{\dot{x}_{nm}^A - \dot{x}_s^R}{V_k} \right) \\ F_{kMT}^{LA} &= \lambda_{nm}^A F_k \left( -1 - \frac{\dot{x}_{nm}^A - \dot{x}_s^L}{V_k} \right) \end{aligned} \quad (8)$$

With  $F_k = 1$  and  $V_k = 1$  (for now on, we are taking  $F_k$  as unit force and  $V_k$  as unit speed), this gives:

$$F_{kMT}^A = \rho_{nm}^A (\dot{x}_s^R - \dot{x}_{nm}^A + 1) - \lambda_{nm}^A (\dot{x}_s^R + \dot{x}_{nm}^A + 1) \quad (9)$$

Eventually, substituting  $\lambda_{nm}^A - \rho_{nm}^A$  with  $\pi_{nm}^A$  and  $\lambda_{nm}^A + \rho_{nm}^A$  with  $|\pi_{nm}^A|$ :

$$F_{kMT}^A = \pi_{nm}^A (\dot{x}_s^R + 1) - |\pi_{nm}^A| \dot{x}_{nm}^A \quad (10)$$

## 2.2 Set of coupled first order differential equations

In the viscous nucleoplasm, inertia is negligible. Newton first principle thus reduces to:  $\sum F = 0$ . This force balance equation can be written for each elements of the spindle. To simplify further, the equations for the right and left SPBs can be combined:

$$\begin{aligned} -\mu_s \dot{x}_s^R + F_z (1 - 2\dot{x}_s^R/V_z) + \sum_{n,m} -\rho_{nm}^A (\dot{x}_s^R - \dot{x}_{nm}^A + 1) &= 0 \text{ for the right SPB} \\ \mu_s \dot{x}_s^R - F_z (1 - 2\dot{x}_s^R/V_z) + \sum_{n,m} \lambda_{nm}^A (\dot{x}_s^R + \dot{x}_{nm}^A + 1) &= 0 \text{ for the left SPB} \end{aligned} \quad (11)$$

The difference of those two expressions gives, with the same substitutions as before:

<sup>1</sup>We want the centromeres to be able to cross each over. In one dimension, this introduces a discontinuity. In the previous version, the 'swap' mechanism was solving this directly (as  $x_A$  and  $x_B$  are exchanged). This is not possible any more, as the 'swap' mechanism is now irrelevant, as there is no preferred side for a given centromere.

$$-2\mu_s \dot{x}_s^R + 2F_z (1 - 2\dot{x}_s^R/V_z) + \sum_{n,m} -(|\pi_{nm}^A| + |\pi_{nm}^B|)(\dot{x}_s^R + 1) + \pi_{nm}^A \dot{x}_{nm}^A + \pi_{nm}^B \dot{x}_{nm}^B = 0 \quad (12)$$

All the equations are gathered together in the system of equations:

$$\mathbf{A}\dot{X} + \mathbf{B}X + C = 0$$

The vector  $X$  has  $1 + 2N(M_k + 1)$  elements and is defined as follow<sup>2</sup>:

$$X = \{x_s^R, \{x_n^A, \{x_{nm}^A\}, x_n^B, \{x_{nm}^B\}\}\} \text{ with } n \in 1 \cdots N \text{ and } m \in 1 \cdots M_k$$

In matrix form, we have:

$$\begin{aligned} X &= \begin{pmatrix} x_s^R \\ x_n^A \\ x_{nm}^A \\ x_n^B \\ x_{nm}^B \end{pmatrix} = \begin{pmatrix} \text{right SPB} \\ \text{centromere } A, n \\ \text{attachment site } A, n, m \\ \text{centromere } B, n \\ \text{attachment site } B, n, m \end{pmatrix} \\ A &= \begin{pmatrix} -2\mu_s - 4F_z/V_z - \sum(|\pi_{nm}^A| + |\pi_{nm}^B|) & \dots & \pi_{nm}^A & \dots & \pi_{nm}^B \\ \dots & -\mu_c - M_k\mu_k & \mu_k & \dots & \dots \\ \pi_{nm}^A & \mu_k & -\mu_k - |\pi_{nm}^A| & \dots & \dots \\ \dots & \dots & -\mu_c - M_k\mu_k & \mu_k & \dots \\ \pi_{nm}^B & \dots & \mu_k & -\mu_k - |\pi_{nm}^B| & \dots \end{pmatrix}, \\ B &= \begin{pmatrix} 0 & \dots & \dots & \dots & \dots \\ \dots & -\kappa_c - M_k\kappa_k & \kappa_k & \kappa_c & \dots \\ \dots & \kappa_k & -\kappa_k & \dots & \dots \\ \dots & \kappa_c & \dots & -\kappa_c - M_k\kappa_k & \kappa_k \\ \dots & \dots & \kappa_k & -\kappa_k & \dots \end{pmatrix} \\ C &= \begin{pmatrix} 2F_z - \sum_{n,m}(|\pi_{nm}^A| + |\pi_{nm}^B|) \\ -\delta_n \kappa_c d_0 \\ \pi_{nm}^A \\ \delta_n \kappa_c d_0 \\ \pi_{nm}^B \end{pmatrix} \text{ with } \delta_n = \begin{cases} 1 & \text{if } x_n^A < x_n^B \\ -1 & \text{if } x_n^A > x_n^B \end{cases} \end{aligned} \quad (13)$$

As is actually done in the python implementation,  $A$  can be decomposed into a time invariant part  $A_0$  and a variable part  $A_t$  with:

$$\begin{aligned} A_0 &= \begin{pmatrix} -2\mu_s - 4F_z/V_z & \dots & \dots & \dots & \dots \\ \dots & -\mu_c - M_k\mu_k & \mu_k & \dots & \dots \\ \dots & \mu_k & -\mu_k & \dots & \dots \\ \dots & \dots & -\mu_c - M_k\mu_k & \mu_k & \dots \\ \dots & \dots & \mu_k & -\mu_k & \dots \end{pmatrix} \\ A_t &= \begin{pmatrix} -\sum(|\pi_{nm}^A| + |\pi_{nm}^B|) & \dots & \pi_{nm}^A & \dots & \pi_{nm}^B \\ \dots & \dots & \dots & \dots & \dots \\ \pi_{nm}^A & \dots & -|\pi_{nm}^A| & \dots & \dots \\ \dots & \dots & \dots & \dots & \dots \\ \pi_{nm}^B & \dots & \dots & -|\pi_{nm}^B| & \dots \end{pmatrix} \end{aligned} \quad (14)$$

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<sup>2</sup>Note that the left SPB is omitted in  $X$ .

